

SEQUENCE LISTING

<110> Kapeller-Libermann, Rosana

<120> 58860, A HUMAN CHOLESTERYL ESTER
HYDROLASE AND USES THEREFOR

<130> MPI2001-026P1RCP1(M)

<150> 60/264,167

<160> 6

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1325

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (16)...(1212)

<400> 1

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tgt gga act tta aat gct ggt gga ttc ctt gat ttg gaa aat gaa gtg   99
Cys Gly Thr Leu Asn Ala Gly Gly Phe Leu Asp Leu Glu Asn Glu Val
          15                20                25

aat cct gag gtg tgg atg aat act agt gaa atc atc atc tac aat ggc   147
Asn Pro Glu Val Trp Met Asn Thr Ser Glu Ile Ile Ile Tyr Asn Gly
          30                35                40

tac ccc agt gaa gag tat gaa gtc acc act gaa gat ggg tat ata ctc   195
Tyr Pro Ser Glu Glu Tyr Glu Val Thr Thr Glu Asp Gly Tyr Ile Leu
          45                50                55                60

ctt gtc aac aga att cct tat ggg cga aca cat gct agg agc aca ggt   243
Leu Val Asn Arg Ile Pro Tyr Gly Arg Thr His Ala Arg Ser Thr Gly
          65                70                75

ccc cgg cca gtt gtg tat atg cag cat gcc ctg ttt gca gac aat gcc   291
Pro Arg Pro Val Val Tyr Met Gln His Ala Leu Phe Ala Asp Asn Ala
          80                85                90

tac tgg ctt gag aat tat gct aat gga agc ctt gga ttc ctt cta gca   339
Tyr Trp Leu Glu Asn Tyr Ala Asn Gly Ser Leu Gly Phe Leu Leu Ala
          95                100                105

gat gca ggt tat gat gta tgg atg gga aac agt cgg gga aac act tgg   387
Asp Ala Gly Tyr Asp Val Trp Met Gly Asn Ser Arg Gly Asn Thr Trp
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tca	aga	aga	cac	aaa	aca	ctc	tca	gag	aca	gat	gag	aaa	ttc	tgg	gcc	435
Ser	Arg	Arg	His	Lys	Thr	Leu	Ser	Glu	Thr	Asp	Glu	Lys	Phe	Trp	Ala	
125					130					135					140	
ttt	agt	ttt	gat	gaa	atg	gcc	aaa	tat	gat	ctc	cca	gga	gta	ata	gac	483
Phe	Ser	Phe	Asp	Glu	Met	Ala	Lys	Tyr	Asp	Leu	Pro	Gly	Val	Ile	Asp	
				145					150					155		
ttc	att	gta	aat	aaa	act	ggg	cag	gag	aaa	ttg	tat	ttc	att	gga	cat	531
Phe	Ile	Val	Asn	Lys	Thr	Gly	Gln	Glu	Lys	Leu	Tyr	Phe	Ile	Gly	His	
			160					165					170			
tca	ctt	ggc	act	aca	ata	ggg	ttt	gta	gcc	ttt	tcc	acc	atg	cct	gaa	579
Ser	Leu	Gly	Thr	Thr	Ile	Gly	Phe	Val	Ala	Phe	Ser	Thr	Met	Pro	Glu	
		175					180					185				
ctg	gca	caa	aga	atc	aaa	atg	aat	ttt	gcc	ttg	ggg	cct	acg	atc	tca	627
Leu	Ala	Gln	Arg	Ile	Lys	Met	Asn	Phe	Ala	Leu	Gly	Pro	Thr	Ile	Ser	
	190					195					200					
ttc	aaa	tat	ccc	acg	ggc	att	ttt	acc	agg	ttt	ttt	cta	ctt	cca	aat	675
Phe	Lys	Tyr	Pro	Thr	Gly	Ile	Phe	Thr	Arg	Phe	Phe	Leu	Leu	Pro	Asn	
205					210					215					220	
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Ser	Ile	Ile	Lys	Ala	Val	Phe	Gly	Thr	Lys	Gly	Phe	Phe	Leu	Glu	Asp	
				225					230					235		
aag	aaa	acg	aag	ata	gct	tct	acc	aaa	atc	tgc	aac	aat	aag	ata	ctc	771
Lys	Lys	Thr	Lys	Ile	Ala	Ser	Thr	Lys	Ile	Cys	Asn	Asn	Lys	Ile	Leu	
			240					245					250			
tgg	ttg	ata	tgt	agc	gaa	ttt	atg	tcc	tta	tgg	gct	gga	tcc	aac	aag	819
Trp	Leu	Ile	Cys	Ser	Glu	Phe	Met	Ser	Leu	Trp	Ala	Gly	Ser	Asn	Lys	
		255					260					265				
aaa	aat	atg	aat	cag	agt	cga	atg	gat	gtg	tat	atg	tca	cat	gct	ccc	867
Lys	Asn	Met	Asn	Gln	Ser	Arg	Met	Asp	Val	Tyr	Met	Ser	His	Ala	Pro	
	270					275					280					
act	ggg	tca	tca	gta	cac	aac	att	ctg	cat	ata	aaa	cag	ctt	tac	cac	915
Thr	Gly	Ser	Ser	Val	His	Asn	Ile	Leu	His	Ile	Lys	Gln	Leu	Tyr	His	
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Ser	Asp	Glu	Phe	Arg	Ala	Tyr	Asp	Trp	Gly	Asn	Asp	Ala	Asp	Asn	Met	
				305					310					315		
aaa	cat	tac	aat	cag	agt	cat	ccc	cct	ata	tat	gac	ctg	act	gcc	atg	1011
Lys	His	Tyr	Asn	Gln	Ser	His	Pro	Pro	Ile	Tyr	Asp	Leu	Thr	Ala	Met	
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aaa	gtg	cct	act	gct	att	tgg	gct	ggg	gga	cat	gat	gtc	ctc	gta	aca	

ccc cag gat gtg gcc agg ata ctc cct caa atc aag agt ctt cat tac 1107
 Pro Gln Asp Val Ala Arg Ile Leu Pro Gln Ile Lys Ser Leu His Tyr
 350 355 360

ttt aag cta ttg cca gat tgg aac cac ttt gat ttt gtc tgg ggc ctc 1155
 Phe Lys Leu Leu Pro Asp Trp Asn His Phe Asp Phe Val Trp Gly Leu
 365 370 375 380

gat gcc cct caa cgg atg tac agt gaa atc ata gct tta atg aag gca 1203
 Asp Ala Pro Gln Arg Met Tyr Ser Glu Ile Ile Ala Leu Met Lys Ala
 385 390 395

tat tcc taa atggaaaaaa aaaaaaaaaa aaaaaaaaaa aaagcggccg 1252
 Tyr Ser *

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 cggccgctaa att 1325

<210> 2

<211> 398

<212> PRT

<213> Homo sapiens

<400> 2

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Trp	Met	Asn	Thr	Ser	Glu	Ile	Ile	Ile	Tyr	Asn	Gly	Tyr	Pro	Ser	Glu
		35					40					45			
Glu	Tyr	Glu	Val	Thr	Thr	Glu	Asp	Gly	Tyr	Ile	Leu	Val	Asn	Arg	
		50				55				60					
Ile	Pro	Tyr	Gly	Arg	Thr	His	Ala	Arg	Ser	Thr	Gly	Pro	Arg	Pro	Val
65				70					75					80	
Val	Tyr	Met	Gln	His	Ala	Leu	Phe	Ala	Asp	Asn	Ala	Tyr	Trp	Leu	Glu
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Asn	Tyr	Ala	Asn	Gly	Ser	Leu	Gly	Phe	Leu	Leu	Ala	Asp	Ala	Gly	Tyr
			100				105					110			
Asp	Val	Trp	Met	Gly	Asn	Ser	Arg	Gly	Asn	Thr	Trp	Ser	Arg	Arg	His
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Lys	Thr	Leu	Ser	Glu	Thr	Asp	Glu	Lys	Phe	Trp	Ala	Phe	Ser	Phe	Asp
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Glu	Met	Ala	Lys	Tyr	Asp	Leu	Pro	Gly	Val	Ile	Asp	Phe	Ile	Val	Asn
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Lys	Thr	Gly	Gln	Glu	Lys	Leu	Tyr	Phe	Ile	Gly	His	Ser	Leu	Gly	Thr
			165					170						175	
Thr	Ile	Gly	Phe	Val	Ala	Phe	Ser	Thr	Met	Pro	Glu	Leu	Ala	Gln	Arg
			180				185						190		
Ile	Lys	Met	Asn	Phe	Ala	Leu	Gly	Pro	Thr	Ile	Ser	Phe	Lys	Tyr	Pro
		195					200				205				
Thr	Gly	Ile	Phe	Thr	Arg	Phe	Phe	Leu	Leu	Pro	Asn	Ser	Ile	Ile	Lys
		210				215				220					
Ala	Val	Phe	Gly	Thr	Lys	Gly	Phe	Phe	Leu	Glu	Asp	Lys	Lys	Thr	Lys
225					230					235				240	
Ile	Ala	Ser	Thr	Lys	Ile	Cys	Asn	Asn	Lys	Ile	Leu	Trp	Leu	Ile	Cys
			245					250						255	

Ala Ile Trp Ala Gly Gly His Asp Val Leu Val Thr Pro Gln Asp Val
 340 345 350

gcc agg ata ctc cct caa atc aag agt ctt cat tac ttt aag cta ttg 1104
 Ala Arg Ile Leu Pro Gln Ile Lys Ser Leu His Tyr Phe Lys Leu Leu
 355 360 365

cca gat tgg aac cac ttt gat ttt gtc tgg ggc ctc gat gcc cct caa 1152
 Pro Asp Trp Asn His Phe Asp Phe Val Trp Gly Leu Asp Ala Pro Gln
 370 375 380

cgg atg tac agt gaa atc ata gct tta atg aag gca tat tcc 1194
 Arg Met Tyr Ser Glu Ile Ile Ala Leu Met Lys Ala Tyr Ser
 385 390 395

<210> 4

<211> 233

<212> PRT

<213> Homo sapiens

<400> 4

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 Glu Ala Leu Leu Asp Ala Leu Gly Leu Asp Lys Pro Val Ile Leu Val
 35 40 45
 Gly His Ser Met Gly Gly Ala Leu Ala Ala Tyr Ala Ala Lys Tyr
 50 55 60
 Pro Glu Glu Arg Val Lys Ala Leu Val Leu Val Ser Thr Pro Ala Pro
 65 70 75 80
 Ala Gly Leu Ser Ser Arg Leu Phe Pro Arg Leu Gly Asn Leu Glu Gly
 85 90 95
 Leu Leu Leu Ala Asn Phe Phe Asn Arg Leu Ser Arg Ser Val Glu Ala
 100 105 110
 Leu Leu Gly Arg Ala Leu Lys Gln Phe Phe Leu Leu Gly Arg Pro Phe
 115 120 125
 Val Ser Asp Phe Leu Lys Gln Ala Glu Asp Trp Leu Ser Ser Leu Ala
 130 135 140
 Arg Pro Gly Glu Thr Asp Gly Gly Asp Gly Leu Leu Gly Tyr Ala Val
 145 150 155 160
 Ala Leu Gly Lys Leu Leu Gln Trp Asp Arg Ser Ala Leu Lys Asp Ile
 165 170 175
 Lys Val Pro Thr Leu Val Ile Trp Gly Asp Asp Asp Pro Leu Val Pro
 180 185 190
 Leu Lys Ala Ser Glu Lys Leu Ser Ala Leu Phe Pro Asn Ala Glu Val
 195 200 205
 Val Val Ile Asp Asp Ala Gly His Leu Ala Leu Leu Glu Lys Pro Glu
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 Glu Val Ala Glu Leu Ile Lys Phe Leu
 225 230

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<211> 127

<212> PRT

<213> Homo sapiens

<400> 5

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20 25 30
Arg Lys His Val Lys Leu Asn Pro Ser His Ser Glu Phe Trp Asp Phe
35 40 45
Ser Trp His Glu Met Gly Met Tyr Asp Leu Pro Ala Met Ile Asp Tyr
50 55 60
Val Leu Glu Thr Thr Gly Gln Glu Lys Leu His Tyr Val Gly His Ser
65 70 75 80
Gln Gly Thr Thr Val Phe Phe Val Met Leu Ser Glu Arg Pro Glu Tyr
85 90 95
Asn Glu Lys Ile Lys Ser Phe His Ala Leu Ala Pro Val Ala Tyr Met
100 105 110
Lys His Val Arg Ser Pro Leu Val Lys Leu Leu Ala Pro Gln Ser

<210> 6

<211> 10

<212> PRT

<213> Homo sapiens

<220>

<221> VARIANT

<222> (1)...(1)

<223> The amino acid at position 1 can be I or V

<223> The amino acid at position 2 can be any amino acid

<221> VARIANT

<222> (3)...(3)

<223> The amino acid at position 3 can be I or V or M or
S or T

<221> VARIANT

<222> (4)...(4)

<223> the amino acid at position 4
can be I or V or M or S or T

<221> VARIANT

<222> (6)...(6)

<223> the amino acid at position 6 can be Y or W or V

<223> The amino acid at position 8
can be any amino acid

<221> VARIANT

<222> (10)...(10)

<223> The amino acid at position 10 can be S or T or A
or C

<400> 6

Leu Xaa Leu Leu Gly His Ser Xaa Gly Gly
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